RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/075,074A_

Source: _,1Fw/6_

Date Processed by STIC: _3/10/05_

ENTERED

IFW16

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   3 <110> APPLICANT: Brown, Arthur M
   4        Wible, Barbara A
   5        Yang, Qing
   7 <120> TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on
Cell Surfaces
   8        and Nucleic Acids That Encode The Same
  10 <130> FILE REFERENCE: 22884/04066
C-->12 <140> CURRENT APPLICATION NUMBER: US/10/075,074A
C-->12 <141> CURRENT FILING DATE: 2002-02-13
  12 <150> PRIOR APPLICATION NUMBER: 09/062,440
  13 <151> PRIOR FILING DATE: 1998-04-17
  15 <150> PRIOR APPLICATION NUMBER: 09/712,495
  16 <151> PRIOR FILING DATE: 2000-11-14
  18 <160> NUMBER OF SEQ ID NOS: 13
  20 <170> SOFTWARE: PatentIn version 3.1
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 1725
  24 <212> TYPE: DNA
  25 <213> ORGANISM: Rattus norvegicus
  27 <220> FEATURE:
  28 <221> NAME/KEY: CDS
  29 <222> LOCATION: (1)..(1725)
  30 <223> OTHER INFORMATION:
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  34 Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
  35 1               5                   10                  15
  37 ggg cct tcc gat ctc tct ttg ctc tct ttg ccc cct ggc acc tct cct        96
  38 Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
  39             20                  25                  30
  41 gta ggc tcc ccc agc ccc ctt gct tcc att cct ccc acc ctc ctg acc       144
  42 Val Gly Ser Pro Ser Pro Leu Ala Ser Ile Pro Pro Thr Leu Leu Thr
  43             35                  40                  45
  45 cct ggc acc ttg ctg ggc cct aag cgt gag gtg gac atg cac cct cct       192
  46 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
  47         50                  55                  60
  49 ctg ccc cag cct gtg cac cct gac gtc acc atg aaa cca ctg ccc ttc       240
  50 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
  51 65                  70                  75                  80
  53 tac gaa gtc tac gga gag ctc atc cgg ccg acc acc ctt gcg tcc acc       288
  54 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
  55                 85                  90                  95
  57 tcc agt cag agg ttt gag gaa gcc cac ttt acc ttt gca ctc act ccc       336
  58 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
```

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59              100                    105                    110
61 cag cag ctg cag cag att ctc aca tcc agg gag gtt ctg cca gga gcc     384
62 Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
63          115                    120                    125
65 aag tgc gat tat acc ata caa gtg cag ctc agg ttc tgt ctc tgt gag     432
66 Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
67     130                    135                    140
69 acc agc tgc ccc cag gag gac tat ttc ccc cct aac ctc ttt gtc aag     480
70 Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
71 145              150                    155                    160
73 gtt aat ggg aaa ctc tgc ccc ctg ccg ggt tac ctc cct cca acc aag     528
74 Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
75              165                    170                    175
77 aat gga gct gag ccc aag agg cct agt cgt cca atc aac atc aca ccc     576
78 Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
79              180                    185                    190
81 ctg gct cgt ctc tca gcc act gtt ccc aac acc ata gtg gtt aac tgg     624
82 Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
83          195                    200                    205
85 tca tct gag ttt gga cgg aat tac tcc ttg tct gtg tac ctg gtg agg     672
86 Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
87     210                    215                    220
89 cag ttg act gca ggg acc ctg cta caa aag ctc aga gcc aag ggt atc     720
90 Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
91 225              230                    235                    240
93 cgg aat cca gac cat tcc cga gca ctg atc aag gag aaa ttg act gct     768
94 Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
95              245                    250                    255
97 gac ccc gac agt gaa gtg gct act aca agt ctc cgg gtg tca ctc atg     816
98 Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
99              260                    265                    270
101 tgc ccg ctg ggg aag atg cgc ctg act gtc cca tgc cgc gct ctc acc     864
102 Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
103          275                    280                    285
105 tgt gcc cac ctg cag agt ttc gat gct gcc ctt tat cta cag atg aat     912
106 Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
107     290                    295                    300
109 gag aaa aag cca aca tgg acg tgc cct gtg tgt gac aag aag gct ccc     960
110 Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
111 305              310                    315                    320
113 tat gag tca ctg att att gat ggt tta ttc atg gaa att ctt aat tcc    1008
114 Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser
115              325                    330                    335
117 tgt tcg gat tgt gat gag atc cag ttc atg gaa gat gga tcc tgg tgt    1056
118 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
119          340                    345                    350
121 cca atg aaa ccc aag aag gag gca tcc gag gtt tgc ccc cca cca ggg    1104
122 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
123          355                    360                    365
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125 tat ggg ctg gat ggt ctc cag tat agc cca gtc cag gag gga aat cag    1152
126 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Glu Gly Asn Gln
127     370                 375                 380
129 tca gag aat aag aag agg gtt gaa gtc att gac ttg aca atc gaa agc    1200
130 Ser Glu Asn Lys Lys Arg Val Glu Val Ile Asp Leu Thr Ile Glu Ser
131 385                 390                 395                 400
133 tca tca gat gag gaa gat ctg ccc ccc acc aag aag cac tgc cct gtt    1248
134 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Pro Val
135                 405                 410                 415
137 acc tcg gct gcc att cca gcc ctt cct gga agc aaa gga gcc ctg acc    1296
138 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Ala Leu Thr
139                 420                 425                 430
141 tct ggt cac cag ccg tct tcg gtg ctg cgg agc cct gca atg ggt aca    1344
142 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr
143             435                 440                 445
145 ctg ggc agt gat ttc ctg tct agt ctc cca cta cat gag tac cca cct    1392
146 Leu Gly Ser Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro
147     450                 455                 460
149 gcc ttc ccg ctg ggg gct gac atc caa ggt tta gat tta ttt tct ttc    1440
150 Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe
151 465                 470                 475                 480
153 ctt cag act gag agt cag cac tac agc cct tca gtt atc act tca cta    1488
154 Leu Gln Thr Glu Ser Gln His Tyr Ser Pro Ser Val Ile Thr Ser Leu
155                 485                 490                 495
157 gat gag cag gac acc ctt ggc cac ttc ttc caa ttc cgg gga acc cct    1536
158 Asp Glu Gln Asp Thr Leu Gly His Phe Phe Gln Phe Arg Gly Thr Pro
159                 500                 505                 510
161 ccc cac ttc ctg ggc cca ctg gcc ccc aca ttg ggg agc tct cac cgc    1584
162 Pro His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Arg
163         515                 520                 525
165 agc gcc act cca gca ccc gct cct ggc cgt gtc agc agc att gtg gct    1632
166 Ser Ala Thr Pro Ala Pro Ala Pro Gly Arg Val Ser Ser Ile Val Ala
167     530                 535                 540
169 cct ggg agt tcc ttg agg gaa ggg cat gga gga ccc ctg cct tcc ggt    1680
170 Pro Gly Ser Ser Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly
171 545                 550                 555                 560
173 ccc tct ttg act ggc tgt cgg tca gac gtc att tcc ttg gac tga        1725
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175                 565                 570
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 574
180 <212> TYPE: PRT
181 <213> ORGANISM: Rattus norvegicus
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189 Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
190             20                  25                  30
193 Val Gly Ser Pro Ser Pro Leu Ala Ser Ile Pro Pro Thr Leu Leu Thr
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Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\03102005\J075074A.raw**

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194         35                    40                   45
197 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
198     50                  55                   60
201 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
202 65                  70                   75                   80
205 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
206                 85                   90                   95
209 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
210             100                  105                  110
213 Gln Gln Leu Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
214             115                  120                  125
217 Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
218         130                  135                  140
221 Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
222 145                 150                  155                  160
225 Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
226                 165                  170                  175
229 Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
230             180                  185                  190
233 Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
234         195                  200                  205
237 Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
238     210                  215                  220
241 Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
242 225                 230                  235                  240
245 Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
246                 245                  250                  255
249 Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
250             260                  265                  270
253 Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
254         275                  280                  285
257 Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
258     290                  295                  300
261 Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
262 305                 310                  315                  320
265 Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Asn Ser
266             325                  330                  335
269 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
270         340                  345                  350
273 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
274     355                  360                  365
277 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Glu Gly Asn Gln
278 370                 375                  380
281 Ser Glu Asn Lys Lys Arg Val Glu Val Ile Asp Leu Thr Ile Glu Ser
282 385                 390                  395                  400
285 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Pro Val
286             405                  410                  415
289 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Ala Leu Thr
290             420                  425                  430
```

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293 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr
294         435             440             445
297 Leu Gly Ser Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro
298     450             455             460
301 Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe
302 465             470             475             480
305 Leu Gln Thr Glu Ser Gln His Tyr Ser Pro Ser Val Ile Thr Ser Leu
306         485             490             495
309 Asp Glu Gln Asp Thr Leu Gly His Phe Phe Gln Phe Arg Gly Thr Pro
310         500             505             510
313 Pro His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Arg
314         515             520             525
317 Ser Ala Thr Pro Ala Pro Ala Pro Gly Arg Val Ser Ser Ile Val Ala
318     530             535             540
321 Pro Gly Ser Ser Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly
322 545             550             555             560
325 Pro Ser Leu Thr Gly Cys Arg Ser Asp Val Ile Ser Leu Asp
326             565             570
329 <210> SEQ ID NO: 3
330 <211> LENGTH: 1725
331 <212> TYPE: DNA
332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (1)..(1725)
337 <223> OTHER INFORMATION:
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340 atg aag atc aaa gag ctt tac cga cga cgc ttt ccc cgg aag acc ctg        48
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342 1           5               10              15
344 ggg ccc tct gat ctc tcc ctt ctc tct ttg ccc cct ggc acc tct cct        96
345 Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
346         20              25              30
348 gta ggc tcc cct ggt cct cta gct ccc att ccc cca acg ctg ttg gcc       144
349 Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala
350         35              40              45
352 cct ggc acc ctg ctg ggc ccc aag cgt gag gtg gac atg cac ccc cct       192
353 Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
354     50              55              60
356 ctg ccc cag cct gtg cac cct gat gtc acc atg aaa cca ttg ccc ttc       240
357 Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
358 65              70              75              80
360 tat gaa gtc tat ggg gag ctc atc cgg ccc acc acc ctt gca tcc act       288
361 Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
362             85              90              95
364 tct agc cag cgg ttt gag gaa gcg cac ttt acc ttt gcc ctc aca ccc       336
365 Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
366         100             105             110
368 cag caa gtg cag cag att ctt aca tcc aga gag gtt ctg cca gga gcc       384
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/10/2005
PATENT APPLICATION: **US/10/075,074A**   TIME: 15:44:33

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\03102005\J075074A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 37,41,48,115,335,381,383,390,415,430,451,489,501,508,513
Seq#:6; Xaa Pos. 528,535,547,548,571
Seq#:10; Xaa Pos. 26,72,74,75,81
Seq#:11; Xaa Pos. 8,23,44,82,94,101,106,121,128,140,141,164

VERIFICATION SUMMARY   DATE: 03/10/2005
PATENT APPLICATION: **US/10/075,074A**   TIME: 15:44:33

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\03102005\J075074A.raw**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:337
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:32
M:341 Repeated in SeqNo=6
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16
M:341 Repeated in SeqNo=10
L:1229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
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